

A. Salimi



RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/717,888

DATE: 08/28/2002
 TIME: 16:15:07

Input Set : N:\Crf3\RULE60\09717888.raw
 Output Set: N:\CRF4\08282002\I717888.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: ANDREW C. HIATT, JULIAN
 6 K.-C. MA, THOMAS LEHNER

8 (ii) TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
 9 PROTEINS IN PLANTS AND THEIR USES

11 (iii) NUMBER OF SEQUENCES: 19

13 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Lyon & Lyon
 16 (B) STREET: 633 West Fifth Street
 17 Suite 4700

18 (C) CITY: Los Angeles

19 (D) STATE: California

20 (E) COUNTRY: U.S.A.

21 (F) ZIP: 90071

23 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 26 storage

27 (B) COMPUTER: IBM Compatible

28 (C) OPERATING SYSTEM: IBM P.C. DOS 5.0

29 (D) SOFTWARE: Word Perfect 5.1

31 (vi) CURRENT APPLICATION DATA:

C--> 33 (A) APPLICATION NUMBER: US/09/717,888

C--> 34 (B) FILING DATE: 20-Nov-2000

35 (C) CLASSIFICATION:

37 (vii) PRIOR APPLICATION DATA:

39 (A) APPLICATION NUMBER: US/08/434,000

40 (B) FILING DATE:

42 (A) APPLICATION NUMBER: 08/367,395

43 (B) FILING DATE: 30-Dec-94

45 (viii) ATTORNEY/AGENT INFORMATION:

47 (A) NAME: Guise, Jeffrey W.

48 (B) REGISTRATION NUMBER: 34,613

49 (C) REFERENCE/DOCKET NUMBER: 212/127

51 (ix) TELECOMMUNICATION INFORMATION:

53 (A) TELEPHONE: (619) 552-8400

54 (B) TELEFAX: (619) 552-0159

55 (C) TELEX: 67-3510

56 SEQUENCE LISTING

59 (2) INFORMATION FOR SEQ ID NO: 1:

61 (i) SEQUENCE CHARACTERISTICS:

63 (A) LENGTH: 3517 base pairs

64 (B) TYPE: nucleic acid

ENTERED

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65          (C) STRANDEDNESS: single
66          (D) TOPOLOGY: linear
67          DESCRIPTION: Rabbit polyimmunoglobulin receptor
68          (ix) FEATURE:
69              (A) NAME/KEY: Coding Sequence
70              (B) LOCATION: 124....2445
71          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
72
73          60
74          GGCCGGGGTT ACGGGCTGGC CAGCAGGCTG TGCCCCGAG TCCGGTCAGCAGGAGGGGAA
75          120
76          GAAGTGGCCT AAAATCTCTC CCGCATCGGC AGCCCAGGCC TAGTGCCCTA CCAGCCACCA
77          168
78          GCC ATG GCT CTC TTC TTG CTC ACC TGC CTG CTG GCT GTC TTT TCA GCG
79          Met Ala Leu Phe Leu Leu Thr Cys Leu Leu Ala Val Phe Ser Ala
80          15
81          1 5 10 15
82          216
83          GCC ACG GCA CAA AGC TCC TTA TTG GGT CCC AGC TCC ATA TTT GGT CCC
84          Ala Thr Ala Gln Ser Ser Leu Leu Gly Pro Ser Ser Ile Phe Gly Pro
85          20 25 30
86          264
87          GGG GAG GTG AAT GTT TTG GAA GGC GAC TCG GTG TCC ATC ACA TGC TAC
88          Gly Glu Val Asn Val Leu Glu Gly Asp Ser Val Ser Ile Thr Cys Tyr
89          35 40 45
90          312
91          TAC CCA ACA ACC TCC GTC ACC CGG CAC AGC CGG AAG TTC TGG TGC CGG
92          Tyr Pro Thr Thr Ser Val Thr Arg His Ser Arg Lys Phe Trp Cys Arg
93          50 55 60
94          360
95          GAA GAG GAG AGC GGC CGC TGC GTG ACG CTT GCC TCG ACC GGC TAC ACG
96          Glu Glu Glu Ser Gly Arg Cys Val Thr Leu Ala Ser Thr Gly Tyr Thr
97          65 70 75
98          408
99          TCC CAG GAA TAC TCC GGG AGA GGC AAG CTC ACC GAC TTC CCT GAT AAA
100          Ser Gln Glu Tyr Ser Gly Arg Gly Lys Leu Thr Asp Phe Pro Asp Lys
101          80 85 90 95
102          456
103          GGG GAG TTT GTG GTG ACT GTT GAC CAA CTC ACC CAG AAC GAC TCA GGG
104          Gly Glu Phe Val Val Thr Val Asp Gln Leu Thr Gln Asn Asp Ser Gly
105          100 105 110
106          504
107          AGC TAC AAG TGT GGC GTG GGA GTC AAC GGC CGT GGC CTG GAC TTC GGT
108          Ser Tyr Lys Cys Gly Val Gly Val Asn Gly Arg Gly Leu Asp Phe Gly
109          115 120 125
110          552
111          GTC AAC GTG CTG GTC AGC CAG AAG CCA GAG CCT GAT GAC GTT GTT TAC
112          Val Asn Val Leu Val Ser Gln Lys Pro Glu Pro Asp Asp Val Val Tyr
113          130 135 140
114          600
115          AAA CAA TAT GAG AGT TAT ACA GTA ACC ATC ACC TGC CCT TTC ACA TAT
116          Lys Gln Tyr Glu Ser Tyr Thr Val Thr Ile Thr Cys Pro Phe Thr Tyr
117          145 150 155
118          648
119          GCG ACT AGG CAA CTA AAG AAG TCC TTT TAC AAG GTG GAA GAC GGG GAA
120          Ala Thr Arg Gln Leu Lys Lys Ser Phe Tyr Lys Val Glu Asp Gly Glu
121          160 165 170 175
122          696
123          CTT GTA CTC ATC ATT GAT TCC AGC AGT AAG GAG GCA AAG GAC CCC AGG
124          Leu Val Leu Ile Ile Asp Ser Ser Ser Lys Glu Ala Lys Asp Pro Arg
125          180 185 190
126          744
127          TAT AAG GGC AGA ATA ACG TTG CAG ATC CAA AGT ACC ACA GCA AAA GAA
128          Tyr Lys Gly Arg Ile Thr Leu Gln Ile Gln Ser Thr Thr Ala Lys Glu
129          195 200 205
130          792
131          TTC ACA GTC ACC ATC AAG CAT TTG CAG CTC AAT GAT GCT GGG CAG TAT

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133	Phe	Thr	Val	Thr	Ile	Lys	His	Leu	Gln	Leu	Asn	Asp	Ala	Gly	Gln	Tyr	
134			210					215					220				
136	GTC	TGC	CAG	AGT	GGA	AGC	GAC	CCC	ACT	GCT	GAA	GAA	CAG	AAC	GTT	GAC	840
137	Val	Cys	Gln	Ser	Gly	Ser	Asp	Pro	Thr	Ala	Glu	Glu	Gln	Asn	Val	Asp	
138		225					230				235						
140	CTC	CGA	CTG	CTA	ACT	CCT	GGT	CTG	CTC	TAT	GGA	AAC	CTG	GGG	GGC	TCG	888
141	Leu	Arg	Leu	Leu	Thr	Pro	Gly	Leu	Leu	Tyr	Gly	Asn	Leu	Gly	Gly	Ser	
142	240					245					250					255	
144	GTG	ACC	TTT	GAA	TGT	GCC	CTG	GAC	TCT	GAA	GAC	GCA	AAC	GCG	GTA	GCA	936
145	Val	Thr	Phe	Glu	Cys	Ala	Leu	Asp	Ser	Glu	Asp	Ala	Asn	Ala	Val	Ala	
146					260					265					270		
148	TCC	TTG	CGC	CAG	GTT	AGG	GGT	GGC	AAT	GTG	GTC	ATT	GAC	AGC	CAG	GGG	984
149	Ser	Leu	Arg	Gln	Val	Arg	Gly	Gly	Asn	Val	Val	Ile	Asp	Ser	Gln	Gly	
150			275						280				285				
152	ACA	ATA	GAT	CCA	GCC	TTC	GAG	GGC	AGG	ATC	CTG	TTC	ACC	AAG	GCT	GAG	1032
153	Thr	Ile	Asp	Pro	Ala	Phe	Glu	Gly	Arg	Ile	Leu	Phe	Thr	Lys	Ala	Glu	
154			290					295					300				
156	AAC	GGC	CAC	TTC	AGT	GTA	GTG	ATC	GCA	GGC	CTG	AGG	AAG	GAA	GAC	ACA	1080
157	Asn	Gly	His	Phe	Ser	Val	Val	Ile	Ala	Gly	Leu	Arg	Lys	Glu	Asp	Thr	
158		305					310				315						
160	GGG	AAC	TAT	CTG	TGC	GGA	GTC	CAG	TCC	AAT	GGT	CAG	TCT	GGG	GAT	GGG	1128
161	Gly	Asn	Tyr	Leu	Cys	Gly	Val	Gln	Ser	Asn	Gly	Gln	Ser	Gly	Asp	Gly	
162	320				325					330					335		
164	CCC	ACC	CAG	CTT	CGG	CAA	CTC	TTC	GTC	AAT	GAA	GAG	ATC	GAC	GTG	TCC	1176
165	Pro	Thr	Gln	Leu	Arg	Gln	Leu	Phe	Val	Asn	Glu	Glu	Ile	Asp	Val	Ser	
166				340					345					350			
168	CGC	AGC	CCC	CCT	GTG	TTG	AAG	GGC	TTT	CCA	GGA	GGC	TCC	GTG	ACC	ATA	1224
169	Arg	Ser	Pro	Pro	Val	Leu	Lys	Gly	Phe	Pro	Gly	Gly	Ser	Val	Thr	Ile	
170			355						360					365			
172	CGC	TGC	CCC	TAC	AAC	CCG	AAG	AGA	AGC	GAC	AGC	CAC	CTG	CAG	CTG	TAT	1272
173	Arg	Cys	Pro	Tyr	Asn	Pro	Lys	Arg	Ser	Asp	Ser	His	Leu	Gln	Leu	Tyr	
174			370					375					380				
176	CTC	TGG	GAA	GGG	AGT	CAA	ACC	CGC	CAT	CTG	CTG	GTG	GAC	AGC	GGC	GAG	1320
177	Leu	Trp	Glu	Gly	Ser	Gln	Thr	Arg	His	Leu	Leu	Val	Asp	Ser	Gly	Glu	
178		385				390				395							
180	GGG	CTG	GTT	CAG	AAA	GAC	TAC	ACA	GGC	AGG	CTG	GCC	CTG	TTC	GAA	GAG	1368
181	Gly	Leu	Val	Gln	Lys	Asp	Tyr	Thr	Gly	Arg	Leu	Ala	Leu	Phe	Glu	Glu	
182	400				405					410					415		
184	CCT	GGC	AAT	GGC	ACC	TTC	TCA	GTC	GTC	CTC	AAC	CAG	CTC	ACT	GCC	GAG	1416
185	Pro	Gly	Asn	Gly	Thr	Phe	Ser	Val	Val	Leu	Asn	Gln	Leu	Thr	Ala	Glu	
186				420					425					430			
188	GAT	GAA	GGC	TTC	TAC	TGG	TGT	GTC	AGC	GAT	GAC	GAT	GAG	TCC	CTG	ACG	1464
189	Asp	Glu	Gly	Phe	Tyr	Trp	Cys	Val	Ser	Asp	Asp	Asp	Glu	Ser	Leu	Thr	
190			435					440					445				
192	ACT	TCG	GTG	AAG	CTC	CAG	ATC	GTT	GAC	GGA	GAA	CCA	AGC	CCC	ACG	ATC	1512
193	Thr	Ser	Val	Lys	Leu	Gln	Ile	Val	Asp	Gly	Glu	Pro	Ser	Pro	Thr	Ile	
194			450				455						460				
196	GAC	AAG	TTC	ACT	GCT	GTG	CAG	GGA	GAG	CCT	GTT	GAG	ATC	ACC	TGC	CAC	1560
197	Asp	Lys	Phe	Thr	Ala	Val	Gln	Gly	Glu	Pro	Val	Glu	Ile	Thr	Cys	His	

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198	465	470	475	
200	TTC CCA TGC AAA TAC TTC TCC TCC GAG AAG TAC TGG TGC AAG TGG AAT	1608		
201	Phe Pro Cys Lys Tyr Phe Ser Ser Glu Lys Tyr Trp Cys Lys Trp Asn			
202	480 485 490 495			
204	GAC CAT GGC TGC GAG GAC CTG CCC ACT AAG CTC AGC TCC AGC GGC GAC	1656		
205	Asp His Gly Cys Glu Asp Leu Pro Thr Lys Leu Ser Ser Ser Gly Asp			
206	500 505 510			
208	CTT GTG AAA TGC AAC AAC AAC CTG GTC CTC ACC CTG ACC TTG GAC TCG	1704		
209	Leu Val Lys Cys Asn Asn Asn Leu Val Leu Thr Leu Thr Leu Asp Ser			
210	515 520 525			
212	GTC AGC GAA GAT GAC GAG GGC TGG TAC TGG TGT GGC GCG AAA GAC GGG	1752		
213	Val Ser Glu Asp Asp Glu Gly Trp Tyr Trp Cys Gly Ala Lys Asp Gly			
214	530 535 540			
216	CAC GAG TTT GAA GAG GTT GCG GCC GTC AGG GTG GAG CTG ACA GAG CCA	1800		
217	His Glu Phe Glu Glu Val Ala Ala Val Arg Val Glu Leu Thr Glu Pro			
218	545 550 555			
220	GCC AAG GTA GCT GTC GAG CCA GCC AAG GTA CCT GTC GAC CCA GCC AAG	1848		
221	Ala Lys Val Ala Val Glu Pro Ala Lys Val Pro Val Asp Pro Ala Lys			
222	560 565 570 575			
224	GCA GCC CCC GCG CCT GCT GAG GAG AAG GCC AAG GCG CGG TGC CCA GTG	1896		
225	Ala Ala Pro Ala Pro Ala Glu Glu Lys Ala Lys Ala Arg Cys Pro Val			
226	580 585 590			
228	CCC AGG AGA AGG CAG TGG TAC CCA TTG TCA AGG AAG CTG AGA ACA AGT	1944		
229	Pro Arg Arg Arg Gln Trp Tyr Pro Leu Ser Arg Lys Leu Arg Thr Ser			
230	595 600 605			
232	TGT CCA GAA CCT CGG CTC CTT GCG GAG GAG GTA GCA GTG CAG AGT GCG	1992		
233	Cys Pro Glu Pro Arg Leu Leu Ala Glu Glu Val Ala Val Gln Ser Ala			
234	610 615 620			
236	GAA GAC CCA GCC AGT GGG AGC AGA GCG TCT GTG GAT GCC AGC AGT GCT	2040		
237	Glu Asp Pro Ala Ser Gly Ser Arg Ala Ser Val Asp Ala Ser Ser Ala			
238	625 630 635			
240	TCG GGA CAA AGC GGG AGT GCC AAA GTA CTG ATC TCC ACC CTG GTG CCC	2088		
241	Ser Gly Gln Ser Gly Ser Ala Lys Val Leu Ile Ser Thr Leu Val Pro			
242	640 645 650 655			
244	TTG GGG CTG GTG CTG GCA GCG GGG GCC ATG GCC GTG GCC ATA GCC AGA	2136		
245	Leu Gly Leu Val Leu Ala Ala Gly Ala Met Ala Val Ala Ile Ala Arg			
246	660 665 670			
248	GCC CGG CAC AGG AGG AAC GTG GAC CGA GTT TCC ATC GGA AGC TAC AGG	2184		
249	Ala Arg His Arg Arg Asn Val Asp Arg Val Ser Ile Gly Ser Tyr Arg			
250	675 680 685			
252	ACA GAC ATT AGC ATG TCA GAC TTG GAG AAC TCC AGG GAG TTC GGA GCC	2232		
253	Thr Asp Ile Ser Met Ser Asp Leu Glu Asn Ser Arg Glu Phe Gly Ala			
254	690 695 700			
256	ATT GAC AAC CCA AGC GCC TGC CCC GAT GCC CGG GAG ACG GCC CTC GGA	2280		
257	Ile Asp Asn Pro Ser Ala Cys Pro Asp Ala Arg Glu Thr Ala Leu Gly			
258	705 710 715			
260	GGA AAG GAT GAG TTA GCG ACG GCC ACC GAG AGC ACC GTG GAG ATT GAG	2328		
261	Gly Lys Asp Glu Leu Ala Thr Ala Thr Glu Ser Thr Val Glu Ile Glu			
262	720 725 730 735			

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264 GAG CCC AAG AAG GCA AAA CGG TCA TCC AAG GAA GAA GCC GAC CTG GCC      2376
265 Glu Pro Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Leu Ala
266              740              745              750
268 TAC TCA GCT TTC CTG CTC CAA TCC AAC ACC ATA GCT GCT GAG CAC CAA      2424
269 Tyr Ser Ala Phe Leu Leu Gln Ser Asn Thr Ile Ala Ala Glu His Gln
270              755              760              765
272 GAT GGC CCC AAG GAG GCC TAG GCACAGCCGG CCACCGCCGC CGCCGCCACC GCCGC      2480
273 Asp Gly Pro Lys Glu Ala
274              770
276 CGCCGCCGCC ACCTGTGAAA ATCACCTTCC AGAATCACGT TGATCCTCGG GGTCCCCAGA      2540
278 GCCGGGGGCT CAACCGCCCT GCACCCCCCA TGTCCCCACC ACCTAAACTT CCCTACCTGT      2600
280 GCCCAGAGGT GTGCTGGTCC CCTCCTCCAC GGCATCCAGG CCTGGCTCAA TGTTCCCGTT      2660
282 GGGGTGGGGT TGTGAGGGGT TCCTACTTGC AGCCCGGTTT TCCCAGAGAG AGCTAAGGAT      2720
284 CCAGGTCCTG AGGAGAGGGC CTCTCGAAGG CAGACAGACC AGAGAGGGGG GAGGAGCCCT      2780
286 TGGATGGGAG GCCAGAGGCG CTTTCCGGCC ACCCCCTCCC TCCCTGCCCC CACCCTCCTT      2840
288 CTTTCATTCA AAAGTCCCAG TGGCTGCTGC CTAGGGTCCA GCGCTGGCC GCACGCCTCC      2900
290 TCGAAGCCGT TGTGCAAACA TCACTGGAGG AAGCCAGGGC TCCTCCCGGG CTGTGTATCC      2960
292 TCACTCAGGC ATCCTGTCCT CCCAGTATC AGGAGATGTC AAGCGTCTGA AGGCTGTGTG      3020
294 CCCTGGGCGT GTCTGCAAGT CACCCAGAC ACATGTTCTC GCCATTTTAC AGATGAGAAC      3080
296 ACTGAGGTTG TACTCAAGG CACCCTGCGA GATGGAGCAA CAGCAAAC TA GATGGGCTTC      3140
298 TGCTGTCCTC TTGGCCAGAG GTCTCTCCAC AGGAGCCCTT GCCCTGTAG GAAGCAGAGT      3200
300 TTTAGAACAT GGAAGAAGAA GAGGGGGATG GCCCTGGACG CTGACCTCTC CCAAGCCCCC      3260
302 ACGGGGGAAG AGGCCCCCTC CTTTCTGTG ACTCTCGGGG ACCTGCGGAG TTGAGCATTC      3320
304 GTGCCCCGTG TGTCTGAAGA GTTCCCAGTG GAAAGAAGAA AAGAGGGTGT TTGTCAAGTG      3380
306 CGGGGAGGGC CTGATCCCCA GACAGCTGAA GTTAAAGGTC CTTGTCCCTG TGAGCTTTAA      3440
308 CCAGCACCTC CGGGCTGACC CTTGCTAACA CATCAGAAAT GTGATTTAAT CATTAAACAT      3500
310 TGTGATTGCC ACTGGGA      3517

```

315 (2) INFORMATION FOR SEQ ID NO: 2:

317 (i) SEQUENCE CHARACTERISTICS:

319 (A) LENGTH: 773 amino acids

320 (B) TYPE: amino acid

321 (C) STRANDEDNESS: single

322 (D) TOPOLOGY: linear

323 DESCRIPTION: Rabbit polyimmunoglobulin receptor

325 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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327 Met Ala Leu Phe Leu Leu Thr Cys Leu Leu Ala Val Phe Ser Ala Ala
328 1              5              10              15
330 Thr Ala Gln Ser Ser Leu Leu Gly Pro Ser Ser Ile Phe Gly Pro Gly
331              20              25              30
333 Glu Val Asn Val Leu Glu Gly Asp Ser Val Ser Ile Thr Cys Tyr Tyr
334              35              40              45
336 Pro Thr Thr Ser Val Thr Arg His Ser Arg Lys Phe Trp Cys Arg Glu
337              50              55              60
339 Glu Glu Ser Gly Arg Cys Val Thr Leu Ala Ser Thr Gly Tyr Thr Ser
340 65              70              75              80
342 Gln Glu Tyr Ser Gly Arg Gly Lys Leu Thr Asp Phe Pro Asp Lys Gly
343              85              90              95
345 Glu Phe Val Val Thr Val Asp Gln Leu Thr Gln Asn Asp Ser Gly Ser
346              100              105              110

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VERIFICATION SUMMARY

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L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]